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RAW SEQUENCE LISTING

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Application Serial Number: 10/539,032
Source: PCT
Date Processed by STIC: 06/22/2005

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PCT

RAW SEQUENCE LISTING

DATE: 06/22/2005

PATENT APPLICATION: US/10/539,032

TIME: 10:30:27

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\06222005\J539032.raw

3 <110> APPLICANT: JAPAN SCIENCE AND TECHNOLOGY AGENCY
 5 <120> TITLE OF INVENTION: Glucose and/or fructose transporter 'NaGLT1' and gene
 thereof
 7 <130> FILE REFERENCE: 4439-4034
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,032
 C--> 10 <141> CURRENT FILING DATE: 2005-06-13
 12 <150> PRIOR APPLICATION NUMBER: JP P2002-363014
 13 <151> PRIOR FILING DATE: 2002-12-13
 15 <160> NUMBER OF SEQ ID NOS: 30
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2173
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Rattus norvegicus
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (111)..(1562)
 28 <400> SEQUENCE: 1
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 31 tggacctcac caaaaaccct ttgtctggag ccaccaagct ggggtcggaa atg gag 116
 32 Met Glu
 33 1
 35 ttc cgt ggg tcc ggg gcc act gct gtt gag cag cac ctc ctc cag tcc 164
 36 Phe Arg Gly Ser Gly Ala Thr Ala Val Glu Gln His Leu Leu Gln Ser
 37 5 10 15
 39 gag acc cca ggg aag aat ggg ctg cag gcc aca tcg agt gac caa gtg 212
 40 Glu Thr Pro Gly Lys Asn Gly Leu Gln Ala Thr Ser Ser Asp Gln Val
 41 20 25 30
 43 gga aga aca ctg cgc tgg ttc acc act gtg gtt ctg aat gct gct ttc 260
 44 Gly Arg Thr Leu Arg Trp Phe Thr Thr Val Val Leu Asn Ala Ala Phe
 45 35 40 45 50
 47 ctg gga atg gga gtg agc gct gct gtg ctg gga ccc aca ttt cca gac 308
 48 Leu Gly Met Gly Val Ser Ala Ala Val Leu Gly Pro Thr Phe Pro Asp
 49 55 60 65
 51 ctg gcc aga aac gtg aac cgg aac atc agc agc ctt tcc gaa atc ttc 356
 52 Leu Ala Arg Asn Val Asn Arg Asn Ile Ser Ser Leu Ser Glu Ile Phe
 53 70 75 80
 55 gtg ggc cga gcc ctc ggc tac ctg ggc ggc tct gtg gtt ggt ggg gtg 404
 56 Val Gly Arg Ala Leu Gly Tyr Leu Gly Gly Ser Val Val Gly Gly Val
 57 85 90 95
 59 ctt ttc gac tgc atg aat cat ttt cta ctt ttg ggg ctg tcc cac ctg 452
 60 Leu Phe Asp Cys Met Asn His Phe Leu Leu Leu Gly Leu Ser His Leu
 61 100 105 110
 63 ctt act gcg gcc ggt ctt tac ctc act cct ttc tgt aaa aca gct gcc 500

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64 Leu Thr Ala Ala Gly Leu Tyr Leu Thr Pro Phe Cys Lys Thr Ala Ala
65 115 120 125 130
67 tta ctg act gcc atg atg tct att acc ggt gtc tca ttt ggt gtt ctg 548
68 Leu Leu Thr Ala Met Met Ser Ile Thr Gly Val Ser Phe Gly Val Leu
69 135 140 145
71 gat aca ggt ggg aat gtc ctc atc ttg gac ctt tgg ggg gac aaa gga 596
72 Asp Thr Gly Gly Asn Val Leu Ile Leu Asp Leu Trp Gly Asp Lys Gly
73 150 155 160
75 gcc cca cat att cag gcc ttg cac ttc agt ttc gcc ttg ggt gcc ttc 644
76 Ala Pro His Ile Gln Ala Leu His Phe Ser Phe Ala Leu Gly Ala Phe
77 165 170 175
79 ctg gct ccc ctg ctg gct aaa ttg gcc tgg ggt acc aca gca tct gct 692
80 Leu Ala Pro Leu Leu Ala Lys Leu Ala Trp Gly Thr Thr Ala Ser Ala
81 180 185 190
83 cag aac cac aca gag cct cag tta gac cgt tca gcc ttg aac cga tcc 740
84 Gln Asn His Thr Glu Pro Gln Leu Asp Arg Ser Ala Leu Asn Arg Ser
85 195 200 205 210
87 ttt gaa gcc gcc tca gac tct gtg ttg gcg gta cct gac gac atg aat 788
88 Phe Glu Ala Ala Ser Asp Ser Val Leu Ala Val Pro Asp Asp Met Asn
89 215 220 225
91 ctt ctg tgg gcg tac gct tcc att gga acc tat gtt cta gta ctt tct 836
92 Leu Leu Trp Ala Tyr Ala Ser Ile Gly Thr Tyr Val Leu Val Leu Ser
93 230 235 240
95 gtc ttc ctg ttt gct cca ttc ttt aaa aag agg tca aag cag aaa aaa 884
96 Val Phe Leu Phe Ala Pro Phe Phe Lys Lys Arg Ser Lys Gln Lys Lys
97 245 250 255
99 tcc gca gcg tct gct cag gga gct cga agg gct aaa tac cac agg gcc 932
100 Ser Ala Ala Ser Ala Gln Gly Ala Arg Arg Ala Lys Tyr His Arg Ala
101 260 265 270
103 ctg cta tgc ctc ctc ttc ctc ttc ttc ttc tac gtg gga gcg gag 980
104 Leu Leu Cys Leu Leu Phe Leu Phe Phe Phe Phe Tyr Val Gly Ala Glu
105 275 280 285 290
107 gtg acc tac ggc tct tac gta ttc tcc ttc gcc acc acc cac gtt ggc 1028
108 Val Thr Tyr Gly Ser Tyr Val Phe Ser Phe Ala Thr Thr His Val Gly
109 295 300 305
111 atg gaa gag agc gag gca gct ggc ttg aac tcc atc ttc tgg ggg acc 1076
112 Met Glu Glu Ser Glu Ala Ala Gly Leu Asn Ser Ile Phe Trp Gly Thr
113 310 315 320
115 ttc gca gcc tgc agg ggc ctg gcc atc ttc ttc gca acg ctc tta cag 1124
116 Phe Ala Ala Cys Arg Gly Leu Ala Ile Phe Phe Ala Thr Leu Leu Gln
117 325 330 335
119 cct ggg acc atg atg gtg ttg tgt aac att ggc agc ctg gcc tca tct 1172
120 Pro Gly Thr Met Met Val Leu Cys Asn Ile Gly Ser Leu Ala Ser Ser
121 340 345 350
123 ttc ttt ctg gtg ctt ttt gac aag agc cct ctt tgc ctc tgg atc gcg 1220
124 Phe Phe Leu Val Leu Phe Asp Lys Ser Pro Leu Cys Leu Trp Ile Ala
125 355 360 365 370
127 tct tct gtg tat gga gcc tca atg gct gcc acg ttt ccc agc ggc atc 1268
128 Ser Ser Val Tyr Gly Ala Ser Met Ala Ala Thr Phe Pro Ser Gly Ile

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131 tcc tgg att gag cag tac acc acc tta act ggg aaa tcc gct gcg ttc 1316
132 Ser Trp Ile Glu Gln Tyr Thr Thr Leu Thr Gly Lys Ser Ala Ala Phe
133          390          395          400
135 att ctg gtt ggt gct gcc ctg gga cta atg gcg act cct gca tta tct 1364
136 Ile Leu Val Gly Ala Ala Leu Gly Leu Met Ala Thr Pro Ala Leu Ser
137          405          410          415
139 gga att ctt cag gga cac tat ccc gat ctg cca gta att ctg tac atg 1412
140 Gly Ile Leu Gln Gly His Tyr Pro Asp Leu Pro Val Ile Leu Tyr Met
141          420          425          430
143 tgt ctg ggc tca gca gta tta aca act gtg tta ttc cct gtg atg tat 1460
144 Cys Leu Gly Ser Ala Val Leu Thr Thr Val Leu Phe Pro Val Met Tyr
145 435          440          445          450
147 aaa gta gcc acc tta cct ctg gat cga aag cag gaa aaa agc atc aac 1508
148 Lys Val Ala Thr Leu Pro Leu Asp Arg Lys Gln Glu Lys Ser Ile Asn
149          455          460          465
151 agt gag ggc cag aaa ata tta ctt tct agc tct agg cta atc aag gaa 1556
152 Ser Glu Gly Gln Lys Ile Leu Leu Ser Ser Ser Arg Leu Ile Lys Glu
153          470          475          480
155 gct aaa tgaaagagga aggggaaagg tgtgaaagca cgtgcgcgcg tgtgtgcgca 1612
156 Ala Lys
158 tgcacgcgca cgcgtaatgg ttttgcggtg gttaaaatga agaatgggac attctctaat 1672
160 aaaaatacaa tagaaatgcc tttatataac ccatagctga ggtctctaag caactctcct 1732
162 gaaatattct gcagccaggg tcttctccag ctgacagggg gcacgcagtc atgaggcacc 1792
164 aggtctcctg agaccctta cactgccctc attgaagtta tctctcagcc catgattcta 1852
166 ggaaagaaaa gtatttctaa aataaaatcc acgacttcca gagatcctgt aagacagctc 1912
168 tgagagatca atgtaactgc cagcaccttc ttcatttcca tgaagtgaga cacagaacag 1972
170 aaatagtttt aaacgtatgc tcctggggct ggtgagatgg cttagtgggt aagagcactg 2032
172 actgctcttc caaaggtcct gagttcaaact cccagcaacc acatggtggc tcacaactat 2092
174 ctgtaatgag atctgatgcc ttcttctggt gtgtctgaag acagcgacag tgtactcata 2152
176 tacatcaaat aaataatatt t 2173
179 <210> SEQ ID NO: 2
180 <211> LENGTH: 484
181 <212> TYPE: PRT
182 <213> ORGANISM: Rattus norvegicus
184 <400> SEQUENCE: 2
185 Met Glu Phe Arg Gly Ser Gly Ala Thr Ala Val Glu Gln His Leu Leu
186 1 5 10 15
188 Gln Ser Glu Thr Pro Gly Lys Asn Gly Leu Gln Ala Thr Ser Ser Asp
189 20 25 30
191 Gln Val Gly Arg Thr Leu Arg Trp Phe Thr Thr Val Val Leu Asn Ala
192 35 40 45
194 Ala Phe Leu Gly Met Gly Val Ser Ala Ala Val Leu Gly Pro Thr Phe
195 50 55 60
197 Pro Asp Leu Ala Arg Asn Val Asn Arg Asn Ile Ser Ser Leu Ser Glu
198 65 70 75 80
200 Ile Phe Val Gly Arg Ala Leu Gly Tyr Leu Gly Gly Ser Val Val Gly
201 85 90 95
203 Gly Val Leu Phe Asp Cys Met Asn His Phe Leu Leu Leu Gly Leu Ser

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204          100          105          110
206 His Leu Leu Thr Ala Ala Gly Leu Tyr Leu Thr Pro Phe Cys Lys Thr
207          115          120          125
209 Ala Ala Leu Leu Thr Ala Met Met Ser Ile Thr Gly Val Ser Phe Gly
210          130          135          140
212 Val Leu Asp Thr Gly Gly Asn Val Leu Ile Leu Asp Leu Trp Gly Asp
213 145          150          155          160
215 Lys Gly Ala Pro His Ile Gln Ala Leu His Phe Ser Phe Ala Leu Gly
216          165          170          175
218 Ala Phe Leu Ala Pro Leu Leu Ala Lys Leu Ala Trp Gly Thr Thr Ala
219          180          185          190
221 Ser Ala Gln Asn His Thr Glu Pro Gln Leu Asp Arg Ser Ala Leu Asn
222          195          200          205
224 Arg Ser Phe Glu Ala Ala Ser Asp Ser Val Leu Ala Val Pro Asp Asp
225          210          215          220
227 Met Asn Leu Leu Trp Ala Tyr Ala Ser Ile Gly Thr Tyr Val Leu Val
228 225          230          235          240
230 Leu Ser Val Phe Leu Phe Ala Pro Phe Phe Lys Lys Arg Ser Lys Gln
231          245          250          255
233 Lys Lys Ser Ala Ala Ser Ala Gln Gly Ala Arg Arg Ala Lys Tyr His
234          260          265          270
236 Arg Ala Leu Leu Cys Leu Leu Phe Leu Phe Phe Phe Tyr Val Gly
237          275          280          285
239 Ala Glu Val Thr Tyr Gly Ser Tyr Val Phe Ser Phe Ala Thr Thr His
240          290          295          300
242 Val Gly Met Glu Glu Ser Glu Ala Ala Gly Leu Asn Ser Ile Phe Trp
243 305          310          315          320
245 Gly Thr Phe Ala Ala Cys Arg Gly Leu Ala Ile Phe Phe Ala Thr Leu
246          325          330          335
248 Leu Gln Pro Gly Thr Met Met Val Leu Cys Asn Ile Gly Ser Leu Ala
249          340          345          350
251 Ser Ser Phe Phe Leu Val Leu Phe Asp Lys Ser Pro Leu Cys Leu Trp
252          355          360          365
254 Ile Ala Ser Ser Val Tyr Gly Ala Ser Met Ala Ala Thr Phe Pro Ser
255          370          375          380
257 Gly Ile Ser Trp Ile Glu Gln Tyr Thr Thr Leu Thr Gly Lys Ser Ala
258 385          390          395          400
260 Ala Phe Ile Leu Val Gly Ala Ala Leu Gly Leu Met Ala Thr Pro Ala
261          405          410          415
263 Leu Ser Gly Ile Leu Gln Gly His Tyr Pro Asp Leu Pro Val Ile Leu
264          420          425          430
266 Tyr Met Cys Leu Gly Ser Ala Val Leu Thr Thr Val Leu Phe Pro Val
267          435          440          445
269 Met Tyr Lys Val Ala Thr Leu Pro Leu Asp Arg Lys Gln Glu Lys Ser
270          450          455          460
272 Ile Asn Ser Glu Gly Gln Lys Ile Leu Leu Ser Ser Arg Leu Ile
273 465          470          475          480
275 Lys Glu Ala Lys
279 <210> SEQ ID NO: 3

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280 <211> LENGTH: 20
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-1 forward
286     primer
288 <400> SEQUENCE: 3
289 tcggaaatgg agttccgtgg                                20
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293 <211> LENGTH: 22
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-2 forward
299     primer
301 <400> SEQUENCE: 4
302 agctgcctta ctgactgccca tg                                22
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 21
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-3 forward
312     primer
314 <400> SEQUENCE: 5
315 tacgtattct ccttcgccac c                                21
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 21
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-4 forward
325     primer
327 <400> SEQUENCE: 6
328 tgtgtaacat tggcagcctg g                                21
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 20
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-5 forward
338     primer
340 <400> SEQUENCE: 7
341 taacccatag ctgaggtctc                                20
344 <210> SEQ ID NO: 8
345 <211> LENGTH: 24
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:

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VERIFICATION SUMMARY

DATE: 06/22/2005

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Input Set : A:\Sequence Listing.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date